IN THE SPECIFICATION:

Please amend the specification as follows:

At page 6, please replace the paragraph beginning "Figure 3A) Maximal average sequence" with the following amended paragraph:

Figure 3A) Maximal average sequence identity of cross-reactive proteins for antibodies targeted against Tpk1p. 3B) Maximal average sequence identity of cross-reactive proteins for antibodies targeted against CDC11p. 3C) Maximal average sequence identity of cross-reactive proteins for antibodies targeted against Rud3p. x-axis = sequence window number, y-axis = maximal average identity. Methods as described in text. Regions of maximal similarity are indicated by arrows. 3D) Sequence alignment of and around the immunogenic peptide region with best matches from each of the cross reacting peptides: Hda1 (SEQ ID NO:42); YMR004W (SEQ ID NO:43); MJR056C (SEQ ID NO:44); YMR110C (SEQ ID NO:45); YLR332W (SEQ ID NO:46); YNR034W (SEQ ID NO:47); YDL204W (SEQ ID NO:48); YDR510W (SEQ ID NO:49); and YDR469W (SEQ ID NO:50). The immunogenic peptide is underlined in the Hda1 sequence. The 8 amino acid window with highest maximal sequence identity between all cross-reacting proteins is depicted in bold.

At page 48, please replace the paragraph beginning "The analysis was followed up" with the following amended paragraph:

The analysis was followed up for the antibody targeted against Hda1, for which it was determined the antibody was raised against a 21 amino acid peptide with the sequence TDGLNNIIEERFEEATDFILD (SEQ ID NO:17). Comparison of this sequence with the sequence cross comparison of the 7 reactive proteins shows that the region of highest similarity (see Figure 3C) is entirely contained within the 21 amino acid sequence of the peptide (Figure 3D). To confirm this peptide as a common epitope on the proteins that cross-react with the anti-Hda1 antibody, arrays were probed with the antibody in the presence of an excess amount of the immunizing peptide; a peptide of similar length but different sequence was used as a control. As shown in Figure 2C, the Hda1 blocking peptide inhibits the interaction of anti-Hda1 with its cognate antigen Ynl021W-Hda1as well to each of the seven cross-reacting proteins. No inhibition of anti-Hda1 binding to these proteins was observed with the control peptide.

At page 53, please replace the paragraph beginning "**Amino Acid Compostion of Hda1 blocking peptide**" with the following amended paragraph:

Amino Acid Compostion of Hda1 blocking peptide. Anti-Hda1 blocking peptide was purchased from Santa Cruz Biotechnologies, Inc (Santa Cruz, CA; 0.2ug/ul in 1XPBS). Peptide was analyzed for amino acid composition using a Beckman 7300 amino acid analyzer at the HHMI Biopolymer Keck Foundation Bioresearch Laboratory at Yale University. Comparison of the amino acid composition with the linear sequence of Hda1 was used to determine the peptide sequence: TDGLNNIIEERFEEATDFILD (SEQ ID NO:17).

At page 56, please replace the paragraph beginning "In order to assess the utility of sequence" with the following amended paragraph:

In order to assess the utility of sequence analysis in predicting cross reactivity, all yeast proteins were searched for either the 8 amino acid epitope core sequence NNIIEERF (SEQ ID NO:1) or the 20/21 amino acid immunogenic peptide sequence TDGLNNIIEERFEEATDFILD (SEQ ID NO:17). The top matches are presented in Table 4. In addition to the observed cross-reactive proteins, a large number of proteins are identified with similarly high sequence conservation which show no empirical evidence of cross reactivity. Thus, although sequence analysis is useful in explaining the observed cross-reactivity, it is clearly insufficient to predict it.

At page 56, please replace **Table 2** with the following amended Table (insertions are indicated by double underscoring):

Table 2. Sequence alignments for the 3 regions of highest homology based on a comprehensive 8 amino acid window sequence comparison. Sequence alignment is shown for 12 amino acids – the 8 amino acid core (bold in all, underlined for reference sequence YNL021W) and 2 amino acids on both N' and C'. Identities are in red.

Sequence	SEQ ID NO.	Protein	Identity (in 8 aa core)
Region 1			
EE**ENSLSTTS**KS	SEQ ID NO:2	YNL021W	
ES**EESSSTNS**VI	SEQ ID NO:3	YDR469W	.625
EQ**ADSSSLTS**FS	SEQ ID NO:4	YLR332W	.5
VM**ENLLTTAG**VS	SEQ ID NO:5	YMR110C	.5
TD**EGSYSTSI**KS	SEQ ID NO:6	YDL204W	.5
Region 2			
FN**EPINDSII**SK	SEQ ID NO:7	YNL021W	
GG**EPINSSVA**SN	SEQ ID NO:8	YLR332W	.625
KN**EPYIDKII**SK	SEQ ID NO:9	YDL204W	.625
FN**ETINKIIE**SK	SEQ ID NO:10	YMR110C	.5
MN**YLIEQSNI**LK	SEQ ID NO:11	YDR469W	.375
Region 3			
GL**NNIIEERF**EE	SEQ ID NO:12	YNL021W	
AS**NDIIEEKF**YD	SEQ ID NO:13	YLR332W	.75
TI**NKIIEEHD**TP	SEQ ID NO:14	YMR110C	.625
NQ**NVKIEESS**EP	SEQ ID NO:15	YDR469W	.5
NL**FNNRHENF**DE	SEQ ID NO:16	YDL204W	.375

At page 57, please replace "**Table 3.** Sequence alignment of the immunogenic" with the following amended Table (insertions are indicated by double underscoring):

Table 3. Sequence alignment of the immunogenic peptide region with best matches from each of the 4 'cross-reactive' proteins. The 8 amino acid core from region 3 (Figure 1) is in bold for all sequences, and underlined in the reference sequence

Sequence	SEQ ID NO.	Protein
TDGL**NNIIEERFE**EATDFILD	SEQ ID NO:17	YNL021W
SVAS**NDIIEEKFY**DEQGNELS	SEQ ID NO:18	YLR332W
KDFH**RNKIESVLN**ETTKLMND	SEQ ID NO:19	YMR110C
FHK**NYNKVVEKTE**PYIDKIIP	SEQ ID NO:20	YDL204W
SSST**NSVIEESSE**PKISKLEN	SEQ ID NO:21	YDR469W

At page 57, please replace "**Table 4.**" with the following amended Table (insertions are indicated by double underscoring):

Table 4.

Sequence	SEQ ID NO.	Protein	Identity
TDGLNNIIEERFEEATDFILD	SEQ ID NO:22	YNL021W	1.000
TNGRNIIIEEIEASRTSFTLY	SEQ ID NO:23	YDR291W	0.476
TDYLKNIIVENSGTSGDEDVD	SEQ ID NO:24	YIL075C	0.429
RDYLNSYIEERLQEEHLDINN	SEQ ID NO:25	YKL201C	0.429
KTDLVNFIEERFKTFCDEELE	SEQ ID NO:26	YKR054C	0.429
TVLENKKIEEGKETAVDREED	SEQ ID NO:27	YKL188C	0.429
IEGLNIISSGTFESLQDFVLQ	SEQ ID NO:28	YNL193W	0.429
TDASNGYDEELPEEEQEFSDD	SEQ ID NO:29	YNL124W	0.429
SYYLNCIIEENFKEMTRKLQR	SEQ ID NO:30	YNL126W	0.429
GQFLENFLELNLNEVTDLIRD	SEQ ID NO:31	YDR481C	0.381
TLSAGNACPGWDEDANDDILD	SEQ ID NO:32	YBR092C	0.381
TDIFKNCLENQFEITNLKILF	SEQ ID NO:33	YKL057C	0.381
DDDDDDEDEEEEEEVTDQLED	SEQ ID NO:34	YFR033C	0.381
VDGKGNETEEDDIKFIKGILD	SEQ ID NO:35	YJL168C	0.381
DDGLPNGITLIGKKFTDYALL	SEQ ID NO:36	YBR208C	0.381
TISLIHEIEKIFEEDIHFEQN	SEQ ID NO:37	YHR184W	0.381
FQGGLDIIKESLEEDPDFLQH	SEQ ID NO:38	YDR098C	0.381
TDYLFDYREVLESLGLDIILD	SEQ ID NO:39	YLR443W	0.381
QFLLSKIIEARISGAFFEIWD	SEQ ID NO:40	YDL231C	0.381
TEFYNNYSMQVREDERDYILD	SEQ ID NO:41	YDL040	0.381

Please amend the specification by entering the Sequence Listing that is being submitted concurrently herewith.